

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Gonsalves, Dennis
Meng, Baozhong

(ii) TITLE OF INVENTION: RUPESTRIS STEM PITTING
ASSOCIATED VIRUS NUCLIEC ACIDS,
PROTEINS, AND THEIR USES

(iii) NUMBER OF SEQUENCES: 54

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
(B) STREET: Clinton Square, P.O. Box 1051
(C) CITY: Rochester
(D) STATE: New York
(E) COUNTRY: U.S.A.
(F) ZIP: 14603

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/047,147
(B) FILING DATE: 20-MAY-1997

(viii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/069,902
(B) FILING DATE: 17-DEC-1997

(ix) ATTORNEY/AGENT INFORMATION:

(A) NAME: Goldman, Michael L.
(B) REGISTRATION NUMBER: 30,727
(C) REFERENCE/DOCKET NUMBER: 19603/1722

(x) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (716) 263-1304
(B) TELEFAX: (716) 263-1600

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8743 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6485 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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TGCAAAGTTG CAAAGCAGG TAGGTCAAAG AAGGAAGGGT GGGATGTAGT AACCTTGAG	4260
GTTCCTCCA GAAAAGTTGC AGGATTGAAG GCTGGCCACT GTGTGATTT TGATGAGGTC	4320
CAGTTGTTTC CTCCTGGATA CATCGATCTA TGCTTGCCTA TTATACGTAG TGATGCTTTC	4380
ATTCACCTG CTGGTGATCC ATGTCAAAGC ACATATGACT CGCAAAAGGA TCGGGCAATT	4440
TTGGCGCTG AGCAGAGTGA CATACTTAGA CTGCTTGAGG GCAAAACGTA TAGGTATAAC	4500
ATAGAAAGCA GGAGGTTGT GAACCCAATG TTCGAATCAA GACTGCCATG TCACTTCAA	4560
AAGGGCTCGA TGACTGCCGC TTTCGCTGAT TATGCAATCT TCCATAATAT GCATGACTTT	4620
CTCCTGGCGA GGTCAAAAGG TCCCTGGAT GCCGTTTGG TTTCCAGTT TGAGGAGAAA	4680
AAGATAGTCC AGTCCTACTT TGGAATGAAA CAGCTCACAC TCACATTGG TGAATCAACT	4740

GGGTTGAATT TCAAAAATGG GGGATTCTC ATATCACATG ATTCCCTTCA CACAGATGAT	4800
CGGC GGTCGGC TTACTGCTTT ATCTCGCTTC AGCCACAATT TGGATTGGT GAACATCACA	4860
GGTCTGAGGG TGGAAAGTTT TCTCTCGCAC TTTGCTGGCA AACCCCTCTA CCATTTTTA	4920
ACAGCCAAAA GTGGGGAGAA TGTCATACGA GATTTGCTCC CAGGTGAGCC TAACTTCTC	4980
AGTGGCTTA ACGTTAGCAT TGGAAAGAAT GAAGGTGTTA GGGAGGAGAA GTTATGTGGT	5040
GACCCATGGT TAAAAGTTAT GCTTTCTG GGTCAAGATG AGGATTGTGA AGTTGAAGAG	5100
ATGGAGTCAG AATGCTAAA TGAAGAATGG TTTAAAACCC ACATCCCCTT GAGTAATCTG	5160
GAGTCAACCA GGGC CAGGTG GGTGGTAAA ATGGCCTTGA AAGAGTATCG GGAGGTGCGT	5220
TGTGGTTATG AAATGACTCA ACAATTCTTT GATGAGCATA GGGGTGGAAC TGGTGAGCAA	5280
CTGAGCAATG CATGTGAGAG GTTGAAAGC ATTACCCAA GGCATAAAGG AAATGATTCA	5340
ATAACCTTCC TCATGGCTGT CCGAAAGCGT CTCAAATTCTT CGAAGCCCCA GGTTGAAGCT	5400
GCCAAACTGA GGC GGGCCAA ACCATATGGG AAATTCTTAT TAGATTCTTT CCTATCCAAA	5460
ATCCCATTGA AAGCCAGTCA TAATTCCATC ATGTTCATG AAGCGGTACA GGAGTTTGAG	5520
GCGAAGAAGG CTAGTAAGAG TGCAGCAACT ATAGAGAAC ATGCAGGTAG GTCATGCAGG	5580
GATTGGTTAT TAGATGTTGC TCTGATTCTT ATGAAGTCAC AACACTGTAC TAAATTGAC	5640
AACAGGCTTA GAGTAGCTAA AGCTGGCAA ACCCTTGCTT GCTTCCAACA TGCTGTTCTG	5700
GTTCGCTTTG CACCCTATAT GAGATACATT GAGAAAAAGC TAATGCAAGC TCTGAAGCCT	5760
AACTTCTACA TCCATTCAAGG GAAAGGTCTG ACGAGCTGAA CGAGTGGTC AGAACTAGAG	5820
GATTCACTGG AATTGCACA GAATCAGACT ACGAAGCCTT TGATGCTTCC CAAGACCCT	5880
TCATCCTAGC ATTGCAATTG CAGATAATGA AATTTTGAGG GTTACCTGAA GATTAAATT	5940
TGGACTATGA ATTCAAAAA ATTCAATTGG GATCAAAGCT CGGATCATTC TCTATAATGA	6000
GGTTTACTGG GGAGGCCAGC ACATTTCTGT TTAACACTAT GGCTAACATG TTGTTCACCT	6060
TTCTGAGGTA CGAACTAACCA GGCTCTGAGT CAATAGCATT TGCAGGTGAT GACATGTGTG	6120
CTAATCGAAG GTTGGCGCTT AAAACAGAGC ATGAGGGTT TCTGAACATG ATTGCGCTTA	6180
AGGCCAAGGT TCAGTTGTT TCCAATCCCA CATTCTGCGG ATGGTGTAA TTTAAGGAAG	6240
GGATCTCAA GAAGCCTCAA TTAATCTGGG AGCGGATATG CATTGCTAGG GAGATGGGCA	6300
ACCTGGAGAA TTGTATTGAC AATTATGCGA TAGAGGTCTC CTATGCATAC CGACTGGGAG	6360
AGCTAGCCAT TGAAATGATG ACCGAGGAAG AAGTGGAGGC CCATTATAAT TGTGTTAGAT	6420
TCTTGGTCAG GAACAAGCAT AAGATGAGAT GCTCAATTTC AGGCCTATTT GAAGCTATTG	6480
ATTAG	6485

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2161 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Ala Leu Ser Tyr Arg Pro Ala Val Glu Glu Val Leu Ala Lys Phe
1 5 10 15

Thr Ser Asp Glu Gln Ser Arg Val Ser Ala Thr Ala Leu Lys Ala Leu
20 25 30

Val Asp Leu Glu Glu Ser Gln His Asn Leu Phe Ser Phe Ala Leu Pro
35 40 45

Asp Arg Ser Lys Glu Arg Leu Ile Ser Ser Gly Ile Tyr Leu Ser Pro
50 55 60

Tyr Ser Phe Arg Pro His Ser His Pro Val Cys Lys Thr Leu Glu Asn
65 70 75 80

His Ile Leu Tyr Asn Val Leu Pro Ser Tyr Val Asn Asn Ser Phe Tyr
85 90 95

Phe Val Gly Ile Lys Asp Phe Lys Leu Gln Phe Leu Lys Arg Arg Asn
100 105 110

Lys Asp Leu Ser Leu Val Ala Leu Ile Asn Arg Phe Val Thr Ser Arg
115 120 125

Asp Val Ser Arg Tyr Gly Ser Glu Phe Val Ile Ser Ser Ser Asp Lys
130 135 140

Ser Ser Gln Val Val Ser Arg Lys Gly Ile Gly Asp Ser Asn Thr Leu
145 150 155 160

Arg Arg Leu Val Pro Arg Val Ile Ser Thr Gly Ala Arg Asn Leu Phe
165 170 175

Leu His Asp Glu Ile His Tyr Trp Ser Ile Ser Asp Leu Ile Asn Phe
180 185 190

Leu Asp Val Ala Lys Pro Ser Met Leu Leu Ala Thr Ala Val Ile Pro
195 200 205

Pro Glu Val Leu Val Gly Ser Pro Glu Ser Leu Asn Pro Trp Ala Tyr
210 215 220

Gln Tyr Lys Ile Asn Gly Asn Gln Leu Leu Phe Ala Pro Asp Gly Asn
225 230 235 240

Trp Asn Glu Met Tyr Ser Gln Pro Leu Ser Cys Arg Tyr Leu Leu Lys
245 250 255

Ala Arg Ser Val Val Leu Pro Asp Gly Ser Arg Tyr Ser Val Asp Ile
260 265 270

Ile His Ser Lys Phe Ser His His Leu Leu Ser Phe Thr Pro Met Gly
275 280 285

Asn Leu Leu Thr Ser Asn Met Arg Cys Phe Ser Gly Phe Asp Ala Ile
290 295 300

Gly Ile Lys Asp Leu Glu Pro Leu Ser Arg Gly Met His Ser Cys Phe
305 310 315 320

Pro Val His His Asp Val Val Thr Lys Ile Tyr Leu Tyr Leu Arg Thr
325 330 335

Leu Lys Lys Pro Asp Lys Glu Ser Ala Glu Ala Lys Leu Arg Gln Leu
340 345 350

Ile Glu Lys Pro Thr Gly Arg Glu Ile Lys Phe Ile Glu Asp Phe Ser
355 360 365

Ser Leu Val Ile Asn Cys Gly Arg Ser Gly Ser Leu Leu Met Pro Asn
370 375 380

Ile Ser Lys Leu Val Ile Ser Phe Phe Cys Arg Met Met Pro Asn Ala
385 390 395 400

Leu Ala Arg Leu Ser Ser Ser Phe Arg Glu Cys Ser Leu Asp Ser Phe
405 410 415

Val Tyr Ser Leu Glu Pro Phe Asn Phe Ser Val Asn Leu Val Asp Ile
420 425 430

Thr Pro Asp Phe Phe Glu His Leu Phe Leu Phe Ser Cys Leu Asn Glu
435 440 445

Leu Ile Glu Glu Asp Val Glu Glu Val Met Asp Asn Ser Trp Phe Gly
450 455 460

Leu Gly Asp Leu Gln Phe Asn Arg Gln Arg Ala Pro Phe Phe Leu Gly
465 470 475 480

Ser Ser Tyr Trp Leu Asn Ser Lys Phe Ser Val Glu His Lys Phe Ser
485 490 495

Gly Thr Ile Asn Ser Gln Ile Met Gln Val Ile Leu Ser Leu Ile Pro
500 505 510

Phe Ser Asp Asp Pro Thr Phe Arg Pro Ser Ser Thr Glu Val Asn Leu
515 520 525

Ala Leu Ser Glu Val Lys Ala Ala Leu Glu Ala Thr Gly Gln Ser Lys
530 535 540

Leu Phe Arg Phe Leu Val Asp Asp Cys Ala Met Arg Glu Val Arg Ser
545 550 555 560

Ser Tyr Lys Val Gly Leu Phe Lys His Ile Lys Ala Leu Thr His Cys
565 570 575

Phe Asn Ser Cys Gly Leu Gln Trp Phe Leu Leu Arg Gln Arg Ser Asn
580 585 590

Leu Lys Phe Leu Lys Asp Arg Ala Ser Ser Phe Ala Asp Leu Asp Cys
595 600 605

Glu Val Ile Lys Val Tyr Gln Leu Val Thr Ser Gln Ala Ile Leu Pro
610 615 620

Glu Ala Leu Leu Ser Leu Thr Lys Val Phe Val Arg Asp Ser Asp Ser
625 630 635 640

Lys Gly Val Ser Ile Pro Arg Leu Val Ser Arg Asn Glu Leu Glu Glu
645 650 655

Leu Ala His Pro Ala Asn Ser Ala Leu Glu Glu Pro Gln Ser Val Asp
660 665 670

Cys Asn Ala Gly Arg Val Gln Ala Ser Val Ser Ser Ser Gln Gln Leu
675 680 685

Ala Asp Thr His Ser Leu Gly Ser Val Lys Ser Ser Ile Glu Thr Ala
690 695 700

Asn Lys Ala Phe Asn Leu Glu Glu Leu Arg Ile Met Ile Arg Val Leu
705 710 715 720

Pro Glu Asp Phe Asn Trp Val Ala Lys Asn Ile Gly Phe Lys Asp Arg
725 730 735

Leu Arg Gly Arg Gly Ala Ser Phe Phe Ser Lys Pro Gly Ile Ser Cys
740 745 750

His Ser Tyr Asn Gly Gly Ser His Thr Ser Leu Gly Trp Pro Lys Phe
755 760 765

Met Asp Gln Ile Leu Ser Ser Thr Gly Gly Arg Asn Tyr Tyr Asn Ser
770 775 780

Cys Leu Ala Gln Ile Tyr Glu Glu Asn Ser Lys Leu Ala Leu His Lys
785 790 795 800

Asp Asp Glu Ser Cys Tyr Glu Ile Gly His Lys Val Leu Thr Val Asn
805 810 815

Leu Ile Gly Ser Ala Thr Phe Thr Ile Ser Lys Ser Arg Asn Leu Val
820 825 830

Gly Gly Asn His Cys Ser Leu Thr Ile Gly Pro Asn Glu Phe Phe Glu
835 840 845

Met Pro Arg Gly Met Gln Cys Asn Tyr Phe His Gly Val Ser Asn Cys
850 855 860

Thr Pro Gly Arg Val Ser Leu Thr Phe Arg Arg Gln Lys Leu Glu Asp
865 870 875 880

Asp Asp Leu Ile Phe Ile Asn Pro Gln Val Pro Ile Glu Leu Asn His
885 890 895

Glu Lys Leu Asp Arg Ser Met Trp Gln Met Gly Leu His Gly Ile Lys
900 905 910

Lys Ser Ile Ser Met Asn Gly Thr Ser Phe Thr Ser Asp Leu Cys Ser
915 920 925

Cys Phe Ser Cys His Asn Phe His Lys Phe Lys Asp Leu Ile Asn Asn
930 935 940

Leu Arg Leu Ala Leu Gly Ala Gln Gly Leu Gly Gln Cys Asp Arg Val
945 950 955 960

Val Phe Ala Thr Thr Gly Pro Gly Leu Ser Lys Val Leu Glu Met Pro
965 970 975

Arg Ser Lys Lys Gln Ser Ile Leu Val Leu Glu Gly Ala Leu Ser Ile
980 985 990

Glu Thr Asp Tyr Gly Pro Lys Val Leu Gly Ser Phe Glu Val Phe Lys
995 1000 1005

Gly Asp Phe His Ile Lys Lys Met Glu Glu Gly Ser Ile Phe Val Ile
1010 1015 1020

Thr Tyr Lys Ala Pro Ile Arg Ser Thr Gly Arg Leu Arg Val His Ser
1025 1030 1035 1040

Ser Glu Cys Ser Phe Ser Gly Ser Lys Glu Val Leu Leu Gly Cys Gln
1045 1050 1055

Ile Glu Ala Cys Ala Asp Tyr Asp Ile Asp Asp Phe Asn Thr Phe Ser
1060 1065 1070

Val Pro Gly Asp Gly Asn Cys Phe Trp His Ser Val Gly Phe Leu Leu
1075 1080 1085

Ser Thr Asp Gly Leu Ala Leu Lys Ala Gly Ile Arg Ser Phe Val Glu
1090 1095 1100

Ser Glu Arg Leu Val Ser Pro Asp Leu Ser Ala Pro Ala Ile Ser Lys
1105 1110 1115 1120

Gln Leu Glu Glu Asn Ala Tyr Ala Glu Asn Glu Met Ile Ala Leu Phe
1125 1130 1135

Cys Ile Arg His His Val Arg Pro Ile Val Ile Thr Pro Glu Tyr Glu
1140 1145 1150

Val Ser Trp Lys Phe Gly Glu Gly Glu Trp Pro Leu Cys Gly Ile Leu
1155 1160 1165

Cys Leu Lys Ser Asn His Phe Gln Pro Cys Ala Pro Leu Asn Gly Cys
1170 1175 1180

Met Ile Thr Ala Ile Ala Ser Ala Leu Gly Arg Arg Glu Val Asp Val
1185 1190 1195 1200

Leu Asn Tyr Leu Cys Arg Pro Ser Thr Asn His Ile Phe Glu Glu Leu
1205 1210 1215

Cys Gln Gly Gly Leu Asn Met Met Tyr Leu Ala Glu Ala Phe Glu
1220 1225 1230

Ala Phe Asp Ile Cys Ala Lys Cys Asp Ile Asn Gly Glu Ile Glu Val
1235 1240 1245

Ile Asn Pro Cys Gly Lys Ile Ser Ala Leu Phe Asp Ile Thr Asn Glu
1250 1255 1260

His Ile Arg His Val Glu Lys Ile Gly Asn Gly Pro Gln Ser Ile Lys
1265 1270 1275 1280

Val Asp Glu Leu Arg Lys Val Lys Arg Ser Ala Leu Asp Phe Leu Ser
1285 1290 1295

Met Asn Gly Ser Lys Ile Thr Tyr Phe Pro Ser Phe Glu Arg Ala Glu
1300 1305 1310

Lys Leu Gln Gly Cys Leu Leu Gly Gly Leu Thr Gly Val Ile Ser Asp
1315 1320 1325

Glu Lys Phe Ser Asp Ala Lys Pro Trp Leu Ser Gly Ile Ser Thr Thr
1330 1335 1340

Asp Ile Lys Pro Arg Glu Leu Thr Val Val Leu Gly Thr Phe Gly Ala
1345 1350 1355 1360

Gly Lys Ser Phe Leu Tyr Lys Ser Phe Met Lys Arg Ser Glu Gly Lys
1365 1370 1375

Phe Val Thr Phe Val Ser Pro Arg Arg Ala Leu Ala Asn Ser Ile Lys
1380 1385 1390

Asn Asp Leu Glu Met Asp Asp Ser Cys Lys Val Ala Lys Ala Gly Arg
1395 1400 1405

Ser Lys Lys Glu Gly Trp Asp Val Val Thr Phe Glu Val Phe Leu Arg
1410 1415 1420

Lys Val Ala Gly Leu Lys Ala Gly His Cys Val Ile Phe Asp Glu Val
1425 1430 1435 1440

Gln Leu Phe Pro Pro Gly Tyr Ile Asp Leu Cys Leu Leu Ile Ile Arg
1445 1450 1455

Ser Asp Ala Phe Ile Ser Leu Ala Gly Asp Pro Cys Gln Ser Thr Tyr
1460 1465 1470

Asp Ser Gln Lys Asp Arg Ala Ile Leu Gly Ala Glu Gln Ser Asp Ile
1475 1480 1485

Leu Arg Leu Leu Glu Gly Lys Thr Tyr Arg Tyr Asn Ile Glu Ser Arg
1490 1495 1500

Arg Phe Val Asn Pro Met Phe Glu Ser Arg Leu Pro Cys His Phe Lys
1505 1510 1515 1520

Lys Gly Ser Met Thr Ala Ala Phe Ala Asp Tyr Ala Ile Phe His Asn
1525 1530 1535

Met His Asp Phe Leu Leu Ala Arg Ser Lys Gly Pro Leu Asp Ala Val
1540 1545 1550

Leu Val Ser Ser Phe Glu Glu Lys Lys Ile Val Gln Ser Tyr Phe Gly
1555 1560 1565

Met Lys Gln Leu Thr Leu Thr Phe Gly Glu Ser Thr Gly Leu Asn Phe
1570 1575 1580

Lys Asn Gly Gly Ile Leu Ile Ser His Asp Ser Phe His Thr Asp Asp
1585 1590 1595 1600

Arg Arg Trp Leu Thr Ala Leu Ser Arg Phe Ser His Asn Leu Asp Leu
1605 1610 1615

Val Asn Ile Thr Gly Leu Arg Val Glu Ser Phe Leu Ser His Phe Ala
1620 1625 1630

Gly Lys Pro Leu Tyr His Phe Leu Thr Ala Lys Ser Gly Glu Asn Val
1635 1640 1645

Ile Arg Asp Leu Leu Pro Gly Glu Pro Asn Phe Phe Ser Gly Phe Asn
1650 1655 1660

Val Ser Ile Gly Lys Asn Glu Gly Val Arg Glu Glu Lys Leu Cys Gly
1665 1670 1675 1680

Asp Pro Trp Leu Lys Val Met Leu Phe Leu Gly Gln Asp Glu Asp Cys
1685 1690 1695

Glu Val Glu Glu Met Glu Ser Glu Cys Ser Asn Glu Glu Trp Phe Lys
1700 1705 1710

Thr His Ile Pro Leu Ser Asn Leu Glu Ser Thr Arg Ala Arg Trp Val
1715 1720 1725

Gly Lys Met Ala Leu Lys Glu Tyr Arg Glu Val Arg Cys Gly Tyr Glu
1730 1735 1740

Met Thr Gln Gln Phe Phe Asp Glu His Arg Gly Gly Thr Gly Glu Gln
1745 1750 1755 1760

Leu Ser Asn Ala Cys Glu Arg Phe Glu Ser Ile Tyr Pro Arg His Lys
1765 1770 1775

Gly Asn Asp Ser Ile Thr Phe Leu Met Ala Val Arg Lys Arg Leu Lys
1780 1785 1790

Phe Ser Lys Pro Gln Val Glu Ala Ala Lys Leu Arg Arg Ala Lys Pro
1795 1800 1805

Tyr Gly Lys Phe Leu Leu Asp Ser Phe Leu Ser Lys Ile Pro Leu Lys
1810 1815 1820

Ala Ser His Asn Ser Ile Met Phe His Glu Ala Val Gln Glu Phe Glu
1825 1830 1835 1840

Ala Lys Lys Ala Ser Lys Ser Ala Ala Thr Ile Glu Asn His Ala Gly
1845 1850 1855

Arg Ser Cys Arg Asp Trp Leu Leu Asp Val Ala Leu Ile Phe Met Lys
1860 1865 1870

Ser Gln His Cys Thr Lys Phe Asp Asn Arg Leu Arg Val Ala Lys Ala
1875 1880 1885

Gly Gln Thr Leu Ala Cys Phe Gln His Ala Val Leu Val Arg Phe Ala
1890 1895 1900

Pro Tyr Met Arg Tyr Ile Glu Lys Lys Leu Met Gln Ala Leu Lys Pro
1905 1910 1915 1920

Asn Phe Tyr Ile His Ser Gly Lys Gly Leu Asp Glu Leu Asn Glu Trp
1925 1930 1935

Val Arg Thr Arg Gly Phe Thr Gly Ile Cys Thr Glu Ser Asp Tyr Glu
1940 1945 1950

Ala Phe Asp Ala Ser Gln Asp His Phe Ile Leu Ala Phe Glu Leu Gln
1955 1960 1965

Ile Met Lys Phe Leu Gly Leu Pro Glu Asp Leu Ile Leu Asp Tyr Glu
1970 1975 1980

Phe Ile Lys Ile His Leu Gly Ser Lys Leu Gly Ser Phe Ser Ile Met
1985 1990 1995 2000

Arg Phe Thr Gly Glu Ala Ser Thr Phe Leu Phe Asn Thr Met Ala Asn
2005 2010 2015

Met Leu Phe Thr Phe Leu Arg Tyr Glu Leu Thr Gly Ser Glu Ser Ile
2020 2025 2030

Ala Phe Ala Gly Asp Asp Met Cys Ala Asn Arg Arg Leu Arg Leu Lys
2035 2040 2045

Thr Glu His Glu Gly Phe Leu Asn Met Ile Cys Leu Lys Ala Lys Val
2050 2055 2060

Gln Phe Val Ser Asn Pro Thr Phe Cys Gly Trp Cys Leu Phe Lys Glu
2065 2070 2075 2080

Gly Ile Phe Lys Lys Pro Gln Leu Ile Trp Glu Arg Ile Cys Ile Ala
2085 2090 2095

Arg Glu Met Gly Asn Leu Glu Asn Cys Ile Asp Asn Tyr Ala Ile Glu
2100 2105 2110

Val Ser Tyr Ala Tyr Arg Leu Gly Glu Leu Ala Ile Glu Met Met Thr
2115 2120 2125

Glu Glu Glu Val Glu Ala His Tyr Asn Cys Val Arg Phe Leu Val Arg
2130 2135 2140

Asn Lys His Lys Met Arg Cys Ser Ile Ser Gly Leu Phe Glu Ala Ile
2145 2150 2155 2160

Asp

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 663 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATGAATAATT TAGTAAAGC ATTGTCAGCA TTTGAGTTG TAGGTGTTT CAGTGTGCTT	60
AAATTTCCAG TAGTCATTCA TAGTGTGCCT GGTAGTGGTA AAAGTAGTTT AATAAGGGAG	120
CTAATTTCCG AGGATGAGAA TTTCATAGCT TTCACAGCAG GTGTTCCAGA CAGCCCTAAT	180
CTCACAGGAA GGTACATTAA GCCTTATTCT CCAGGGTGTG CAGTGCCAGG GAAAGTTAAT	240
ATACTTGATG AGTACTTGTC CGTCCAAGAT TTTTCAGGTT TTGATGTGCT GTTCTCGGAC	300
CCATACCAAA ACATCAGCAT TCCTAAAGAG GCACATTCA TCAAGTCAAA AACTTGTAGG	360
TTTGGCGTGA ATACTTGCAA ATATCTTCC TCCTTCGGTT TTAAGGTTAG CAGTGACGGT	420
TTGGACAAAG TCATTGTGGG GTCGCCTTTT ACACTAGATG TTGAAGGGGT GCTAATATGC	480
TTTGGTAAGG AGGCAGTGGA TCTCGCTGTT GCGCACAACT CTGAATTCAA ATTACCTTGT	540
GAAGTTAGAG GTTCAACTTT TAACGTCGTA ACTCTTTGA AATCAAGAGA TCCAACCCCA	600
GAGGATAGGC ACTGGTTTA CATTGCTGCT ACAAGACACA GGGAGAAATT GATAATCATG	660
CAG	663

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 221 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Asn Asn Leu Val Lys Ala Leu Ser Ala Phe Glu Phe Val Gly Val			
1	5	10	15

Phe Ser Val Leu Lys Phe Pro Val Val Ile His Ser Val Pro Gly Ser
20 25 30

Gly Lys Ser Ser Leu Ile Arg Glu Leu Ile Ser Glu Asp Glu Asn Phe
35 40 45

Ile Ala Phe Thr Ala Gly Val Pro Asp Ser Pro Asn Leu Thr Gly Arg
50 55 60

Tyr Ile Lys Pro Tyr Ser Pro Gly Cys Ala Val Pro Gly Lys Val Asn
65 70 75 80

Ile Leu Asp Glu Tyr Leu Ser Val Gln Asp Phe Ser Gly Phe Asp Val
85 90 95

Leu Phe Ser Asp Pro Tyr Gln Asn Ile Ser Ile Pro Lys Glu Ala His
100 105 110

Phe Ile Lys Ser Lys Thr Cys Arg Phe Gly Val Asn Thr Cys Lys Tyr
115 120 125

Leu Ser Ser Phe Gly Phe Lys Val Ser Ser Asp Gly Leu Asp Lys Val
130 135 140

Ile Val Gly Ser Pro Phe Thr Leu Asp Val Glu Gly Val Leu Ile Cys
145 150 155 160

Phe Gly Lys Glu Ala Val Asp Leu Ala Val Ala His Asn Ser Glu Phe
165 170 175

Lys Leu Pro Cys Glu Val Arg Gly Ser Thr Phe Asn Val Val Thr Leu
180 185 190

Leu Lys Ser Arg Asp Pro Thr Pro Glu Asp Arg His Trp Phe Tyr Ile
195 200 205

Ala Ala Thr Arg His Arg Glu Lys Leu Ile Ile Met Gln
210 215 220

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATGCCTTTC AGCAGCCTGC GAATTGGGCA AAAACCATAA CTCCATTGAC AGTTGGCTTG 60
GGCATTGGGC TTGTGCTGCA TTTTCTGAGG AAGTCAAATC TACCTTATTC AGGGGACAAC 120
ATCCATCAAT TCCCTCACGG TGGGCGTTAC AGGGACGGTA CAAAAAGTAT AACTTACTGT 180

GGTCCAAAGC AATCCTTCCC CAGCTCTGGG ATATTCGGCC AATCTGAGAA TTTTGTGCC	240
TTAATGCTTG TCATAGGTCT AATCGCATTG ATACATGTAT TGTCTGTTG GAATTCTGGT	300
CTTGGTAGGA ATTGTAATTG CCATCAAAT CCTTGCTCAT GTAGACAGCA G	351

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 117 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Pro Phe Gln Gln Pro Ala Asn Trp Ala Lys Thr Ile Thr Pro Leu			
1	5	10	15
Thr Val Gly Leu Gly Ile Gly Leu Val Leu His Phe Leu Arg Lys Ser			
20	25	30	
Asn Leu Pro Tyr Ser Gly Asp Asn Ile His Gln Phe Pro His Gly Gly			
35	40	45	
Arg Tyr Arg Asp Gly Thr Lys Ser Ile Thr Tyr Cys Gly Pro Lys Gln			
50	55	60	
Ser Phe Pro Ser Ser Gly Ile Phe Gly Gln Ser Glu Asn Phe Val Pro			
65	70	75	80
Leu Met Leu Val Ile Gly Leu Ile Ala Phe Ile His Val Leu Ser Val			
85	90	95	
Trp Asn Ser Gly Leu Gly Arg Asn Cys Asn Cys His Pro Asn Pro Cys			
100	105	110	
Ser Cys Arg Gln Gln			
115			

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 240 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATGTATTGTC TGTTTGAAT TCTGGTCTTG GTAGGAATTG TAATTGCCAT CCAAATCCTT	60
GCTCATGTAG ACAGCAGTAG TGGCAACCAC CAAGGTTGCT TCATTAGGGC CACTGGAGAG	120
TCAATTGAA TTGAAAATG CGGCCAAGT GAGGCCCTTG CATCCACTGT GAAGGAGGTG	180
CTGGGAGGTT TGAAGGCTTT AGGGGTTAGC CGTGCTGTTG AAGAAATTGA TTATCATTGT	240

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 80 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Tyr Cys Leu Phe Gly Ile Leu Val Leu Val Gly Ile Val Ile Ala			
1	5	10	15
Ile Gln Ile Leu Ala His Val Asp Ser Ser Ser Gly Asn His Gln Gly			
20	25	30	
Cys Phe Ile Arg Ala Thr Gly Glu Ser Ile Leu Ile Glu Asn Cys Gly			
35	40	45	
Pro Ser Glu Ala Leu Ala Ser Thr Val Lys Glu Val Leu Gly Gly Leu			
50	55	60	
Lys Ala Leu Gly Val Ser Arg Ala Val Glu Glu Ile Asp Tyr His Cys			
65	70	75	80

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 777 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATGGCAAGTC AAATTGGGAA ACTCCCCGGT GAATCAAATG AGGCTTTGA AGCCCGGCTA	60
AAATCGCTGG AGTTAGCTAG AGCTCAAAAG CAGCCGGAAG GTTCTAATGC ACCACCTACT	120

CTCAGTGGCA TTCTTGCCAA ACGCAAGAGG ATTATAGAGA ATGCACTTTC AAAGACGGTG	180
GACATGAGGG AGGTTTGAA ACACGAAACG GTGGTGATT CCCCAAATGT CATGGATGAA	240
GGTGCAATAG ACGAGCTGAT TCGTGCATTT GGTGAATCTG GCATAGCTGA AAGCGTGCAA	300
TTTGATGTGG CCATAGATAT AGCACGTCAC TGCTCTGATG TTGGTAGCTC CCAGAGTTCA	360
ACCCCTGATTG GCAAGAGTCC ATTTTGTGAC CAAACAGAT CAGAAATAGC TGGGATTATA	420
AGGGAGGTGA CCACATTACG TAGATTTGC ATGTACTATG CAAAAATCGT GTGGAACATC	480
CATCTGGAGA CGGGGATACC ACCAGCTAAC TGGGCCAAGA AAGGATTAA TGAGAATGAA	540
AAGTTTGCAG CCTTGATTT TTTCTGGGA GTCACAGATG AGAGTGCCT TGAAACAAAG	600
GGTGGAAATTA AAAGAGCTCC AACGAAAGCT GAGATGGTTG CTAATATCGC CTCTTTGAG	660
GTTCAAGTGC TCAGACAAGC TATGGCTGAA GGCAAGCGGA GTTCCAACCT TGGAGAGATT	720
AGTGGTGGAA CGGCTGGTGC ACTCATCAAC AACCCCTTT CAAATGTTAC ACATGAA	777

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 259 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Ala Ser Gln Ile Gly Lys Leu Pro Gly Glu Ser Asn Glu Ala Phe			
1	5	10	15
Glu Ala Arg Leu Lys Ser Leu Glu Leu Ala Arg Ala Gln Lys Gln Pro			
20	25	30	
Glu Gly Ser Asn Ala Pro Pro Thr Leu Ser Gly Ile Leu Ala Lys Arg			
35	40	45	
Lys Arg Ile Ile Glu Asn Ala Leu Ser Lys Thr Val Asp Met Arg Glu			
50	55	60	
Val Leu Lys His Glu Thr Val Val Ile Ser Pro Asn Val Met Asp Glu			
65	70	75	80
Gly Ala Ile Asp Glu Leu Ile Arg Ala Phe Gly Glu Ser Gly Ile Ala			
85	90	95	
Glu Ser Val Gln Phe Asp Val Ala Ile Asp Ile Ala Arg His Cys Ser			
100	105	110	
Asp Val Gly Ser Ser Gln Ser Ser Thr Leu Ile Gly Lys Ser Pro Phe			
115	120	125	

Cys Asp Leu Asn Arg Ser Glu Ile Ala Gly Ile Ile Arg Glu Val Thr
130 135 140

Thr Leu Arg Arg Phe Cys Met Tyr Tyr Ala Lys Ile Val Trp Asn Ile
145 150 155 160

His Leu Glu Thr Gly Ile Pro Pro Ala Asn Trp Ala Lys Lys Gly Phe
165 170 175

Asn Glu Asn Glu Lys Phe Ala Ala Phe Asp Phe Phe Leu Gly Val Thr
180 185 190

Asp Glu Ser Ala Leu Glu Pro Lys Gly Gly Ile Lys Arg Ala Pro Thr
195 200 205

Lys Ala Glu Met Val Ala Asn Ile Ala Ser Phe Glu Val Gln Val Leu
210 215 220

Arg Gln Ala Met Ala Glu Gly Lys Arg Ser Ser Asn Leu Gly Glu Ile
225 230 235 240

Ser Gly Gly Thr Ala Gly Ala Leu Ile Asn Asn Pro Phe Ser Asn Val
245 250 255

Thr His Glu

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2680 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGCTGGCAA ACTTTGGCCT GCTTCAACA CGCCGTCTTG GTTCGCTTTG CACCCCTACAT 60
GCGATACATT GAAAAGAACG TTGTGCAGGC ATTGAAACCA AATTCTACA TTCATTCTGG 120
CAAAGGTCTT GATGAGCTAA GTGAATGGGT TAGAGCCAGA GGTTTCACAG GTGTGTGTAC 180
TGAGTCAGAC TATGAAGCTT TTGATGCATC CCAAGATCAT TTCATCCTGG CATTGAACT 240
GCAAATCATG AGATTTTAG GACTGCCAGA AGATCTGATT TTAGATTATG AGTTCATCAA 300
AATTCATCTT GGGTCAAAGC TTGGCTCTT TGCAATTATG AGATTCACAG GTGAGGCAAG 360
CACCTTCCTA TTCAATACTA TGGCCAACAT GCTATTCACT TTCCTGAGGT ATGAGTTGAC 420
AGGTTCTGAA TCAATTGCAT TTGCTGGAGA TGATATGTGT GCTAATCGCA GGTAAAGACT 480
CAAGACTGAG CACGCCGGCT TTCTAACAT GATCTGTCTC AAAGCTAAGG TGCAGTTGT 540

CACAAATCCC ACCTTCTGTG GATGGTGTGTT GTTAAAGAG GGAATCTTA AAAAACCCA	600
GCTCATTGG GAAAGGATCT GCATTGCTAG GGAAATGGGT AACTTGGACA ATTGCATTGA	660
CAATTACGCA ATTGAGGTGT CTTATGCTTA CAGACTGGGG GAATTGTCCA TAGGCGTGAT	720
GAAGTGGAG GAAAGTTGAAG CACATTCTAA CTGCGTGCCT TTCCCTGGTTC GCAATAAGCA	780
CAAGATGAGG TGCTCAATT TGAGTAAATT GTTTAGGCCT TAAGTGTGTTG	840
GCATGGTGTG AGTATTATGA ATAACCTTAGT CAAAGCTTTG TCTGCTTTG AATTGTTGG	900
TGTGTTTGT GTACTTAAAT TTCCAGTTGT TGTTCACAGT GTTCCAGGTA GCGGTAAAAG	960
TAGCCTAATA AGGGAGCTCA TTTCTGAAGA CGAGGCTTT GTGGCCTTA CAGCAGGTGT	1020
GCCAGACAGT CCAAATCTGA CAGGGAGGTA CATCAAGCCC TACGCTCCAG GGTGTGCAGT	1080
GCAAGGGAAA ATAAACATAC TTGATGAGTA CTTGTCTGTC TCTGATACTT CTGGCTTGAA	1140
TGTGCTGTTG TCAGACCCTT ACCAGAATGT CAGCATTCCA AGGGAGGCAC ACTTCATAAA	1200
AACCAAAACC TGTAGGTTG GTACCAACAC CTGCAAGTAC CTTCAATCTT TTGGCTTAA	1260
TGTTGTAGT GATGGGGTGG ATAAAGTTGT TGAGGTCG CCATTGAAC TGGAGGTTGA	1320
GGGGGTTCTC ATTGCTTG GAAAGGAGGC TGAGATCTA GCAGTTGCAC ACAATTCTGA	1380
CTTCAAGTTG CCCTGCGAGG TGCGGGTTC AACATTGAC GTTGTAACTGT TATTGAAGTC	1440
CAGGGATCCA ACTTCAGAAG ATAAGCATTG GTTCTACGTT GCAGCCACAA GGCATCGAAG	1500
TAAACTGATA ATAATGCAGT AAAATGCCCTT TTCAGCAACC TGCCAACGG GCTAAGACCA	1560
TAACCTCCATT AACTATTGGT TTGGGCATTG GGTTGGTTCT GCACCTCTTA AGGAAATCAA	1620
ATCTGCCATA TTCAGGAGAC AATATTCAAC AGTTCCCACA CGGAGGGCAT TACAGGGACG	1680
GCACGAAGAG TATAACCTAT TGTGGCCCTA GGCAGTCATT CCCAAGCTCA GGAATATTG	1740
GTCAGTCTGA AAATTCGTA CCTCTAATAT TGGTCGTGAC TCTGGTCGCT TTTATACATG	1800
CGTTATCTCT TTGGAATTCT GGTCTAGTA GGAGTTGCAA TTGCCATCCA AATCCTTGCA	1860
CATGTAGACA GCAGTAGTGG CAACCATCAA GGCTGTTCA TAAGAGCCAC CGGGGAGTCA	1920
ATAGTAATTG AGAATTGTGG GCCGAGCGAG GCCCTAGCTG CTACAGTCAC AGAGGTGTTG	1980
GGCGGTCTAA AGGCTTTAGG GTAGGCCAA AAGGTTGATG AAATTAATTA CAGTTGTTGA	2040
GACAGTTGAA TGGCAAGTCA AGTTGGAAAA TTGCCTGGCG AATCAAATGA AGCATATGAG	2100
GCTAGACTCA AGGCTTTAGA GTTAGCAAGG GCCCAAAAG CTCCAGAAGT CTCCAACCAA	2160
CCTCCCACAC TTGGAGGCAT TCTAGCCAAA AGGAAAAGAG TGATTGAGAA TGCACCTCTA	2220
AAGACAGTGG ATATGCGTGA AGTCTTAAGG CATGAATCTG TTGTACTCTC CCCGAATGTA	2280
ATGGACGAGG GAGCAATAGA CGAGCTGATT CGTGCCTTG GGGAGTCGGG CATAGCTGAA	2340

AATGTGCAGT TTGATGTTGC AATAGACATT GCTGCCACT GTTCTGATGT GGGGAGCTCT	2400
CAGAGGTCAA CCCTTATTGG TAAAAGCCCC TTCTGTGAGT TAAATAGGTC TGAAATTGCC	2460
GGAATAATAA GGGAGGTGAC CACGCTGCGC AGATTTGCA TGTACTACGC AAAGATTGTG	2520
TGGAACATCC ATTTGGAGAC GGGAAATACCA CCAGCTAATT GGGCCAAGAA AGGATTTAAT	2580
GAGAATGAAA AGTTTGCAGC CTTTGACTTC TTCCTGGAG TCACAGATGA AAGCGCGCTT	2640
GAGCCTAAGG GTGGAGTCAA GAGAGCTCCA ACAAAAGCAG	2680

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 767 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ATGCGATACA TTGAAAAGAA GCTTGTGCAG GCATTGAAAC CAAATTTCTA CATTCAATTCT	60
GGCAAAGGTC TTGATGAGCT AAGTGAATGG GTTAGAGCCA GAGGTTTCAC AGGTGTGTGT	120
ACTGAGTCAG ACTATGAAGC TTTTGATGCA TCCCAAGATC ATTCATCCT GGCATTTGAA	180
CTGCAAATCA TGAGATTTT AGGACTGCCA GAAGATCTGA TTTTAGATTA TGAGTTCATC	240
AAAATTCAATC TTGGGTCAAA GCTTGGCTCT TTTGCAATTA TGAGATTAC AGGTGAGGCA	300
AGCACCTTCC TATTCAATAC TATGCCAAC ATGCTATTCA CTTTCCTGAG GTATGAGTTG	360
ACAGGTTCTG AATCAATTGC ATTTGCTGGA GATGATATGT GTGCTAATCG CAGGTTAAGA	420
CTCAAGACTG AGCACGCCGG CTTTCTAAAC ATGATCTGTC TCAAAGCTAA GGTGCAGTT	480
GTCACAAATC CCACCTTCTG TGGATGGTGT TTGTTAAAG AGGAAATCTT TAAAAAAACCC	540
CAGCTCATTG GGGAAAGGAT CTGCATTGCT AGGGAAATGG GTAACCTGGA CAATTGCATT	600
GACAATTACG CAATTGAGGT GTCTTATGCT TACAGACTTG GGGAAATTGTC CATAGGCGTG	660
ATGACTGAGG AGGAAGTTGA AGCACATTCT AACTGCGTGC GTTCCCTGGT TCGCAATAAG	720
CACAAGATGA GGTGCTCAAT TTCTGGTTG TTTGAAGTAA TTGTTTA	767

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 255 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Arg Tyr Ile Glu Lys Lys Leu Val Gln Ala Leu Lys Pro Asn Phe
1 5 10 15

Tyr Ile His Ser Gly Lys Gly Leu Asp Glu Leu Ser Glu Trp Val Arg
20 25 30

Ala Arg Gly Phe Thr Gly Val Cys Thr Glu Ser Asp Tyr Glu Ala Phe
35 40 45

Asp Ala Ser Gln Asp His Phe Ile Leu Ala Phe Glu Leu Gln Ile Met
50 55 60

Arg Phe Leu Gly Leu Pro Glu Asp Leu Ile Leu Asp Tyr Glu Phe Ile
65 70 75 80

Lys Ile His Leu Gly Ser Lys Leu Gly Ser Phe Ala Ile Met Arg Phe
85 90 95

Thr Gly Glu Ala Ser Thr Phe Leu Phe Asn Thr Met Ala Asn Met Leu
100 105 110

Phe Thr Phe Leu Arg Tyr Glu Leu Thr Gly Ser Glu Ser Ile Ala Phe
115 120 125

Ala Gly Asp Asp Met Cys Ala Asn Arg Arg Leu Arg Leu Lys Thr Glu
130 135 140

His Ala Gly Phe Leu Asn Met Ile Cys Leu Lys Ala Lys Val Gln Phe
145 150 155 160

Val Thr Asn Pro Thr Phe Cys Gly Trp Cys Leu Phe Lys Glu Gly Ile
165 170 175

Phe Lys Lys Pro Gln Leu Ile Trp Glu Arg Ile Cys Ile Ala Arg Glu
180 185 190

Met Gly Asn Leu Asp Asn Cys Ile Asp Asn Tyr Ala Ile Glu Val Ser
195 200 205

Tyr Ala Tyr Arg Leu Gly Glu Leu Ser Ile Gly Val Met Thr Glu Glu
210 215 220

Glu Val Glu Ala His Ser Asn Cys Val Arg Phe Leu Val Arg Asn Lys
225 230 235 240

His Lys Met Arg Cys Ser Ile Ser Gly Leu Phe Glu Val Ile Val
245 250 255

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 666 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ATGAATAACT TAGTCAAAGC TTTGTCTGCT TTTGAATTG TTGGTGTGTT TTGTGTACTT	60
AAATTTCAG TTGTTGTTCA CAGTGTCCA GGTAGCGGTA AAAGTAGCCT AATAAGGGAG	120
CTCATTCTG AAGACGAGGC TTTTGTGCC TTTACAGCAG GTGTGCCAGA CAGTCCAAAT	180
CTGACAGGGA GGTACATCAA GCCCTACGCT CCAGGGTGTG CAGTGCAAGG GAAAATAAAC	240
ATACTTGATG AGTACTTGTC TGTCTCTGAT ACTTCTGGCT TTGATGTGCT GTTCTCAGAC	300
CCTTACCAGA ATGTCAGCAT TCCAAGGGAG GCACACTTCA TAAAAACCAA AACCTGTAGG	360
TTTGGTACCA ACACCTGCAA GTACCTCAA TCTTTGGCT TTAATGTTG TAGTGATGGG	420
GTGGATAAAG TTGTTGTAGG GTCGCCATT GAACGGGAGG TTGAGGGGGT TCTCATTGC	480
TTTGGAAAGG AGGCTGTAGA TCTAGCAGTT GCACACAATT CTGACTTCAA GTTGCCTGC	540
GAGGTGCCGG GTTCAACATT TGACGTTGTA ACGTTATTGA AGTCCAGGGA TCCAACATTCA	600
GAAGATAAGC ATTGGTTCTA CGTTGCAGCC ACAAGGCATC GAAGTAAACT GATAATAATG	660
CAGTAA	666

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 221 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met Asn Asn Leu Val Lys Ala Leu Ser Ala Phe Glu Phe Val Gly Val			
1	5	10	15
Phe Cys Val Leu Lys Phe Pro Val Val Val His Ser Val Pro Gly Ser			
20	25	30	
Gly Lys Ser Ser Leu Ile Arg Glu Leu Ile Ser Glu Asp Glu Ala Phe			
35	40	45	

Val Ala Phe Thr Ala Gly Val Pro Asp Ser Pro Asn Leu Thr Gly Arg
50 55 60

Tyr Ile Lys Pro Tyr Ala Pro Gly Cys Ala Val Gln Gly Lys Ile Asn
65 70 75 80

Ile Leu Asp Glu Tyr Leu Ser Val Ser Asp Thr Ser Gly Phe Asp Val
85 90 95

Leu Phe Ser Asp Pro Tyr Gln Asn Val Ser Ile Pro Arg Glu Ala His
100 105 110

Phe Ile Lys Thr Lys Thr Cys Arg Phe Gly Thr Asn Thr Cys Lys Tyr
115 120 125

Leu Gln Ser Phe Gly Phe Asn Val Cys Ser Asp Gly Val Asp Lys Val
130 135 140

Val Val Gly Ser Pro Phe Glu Leu Glu Val Glu Gly Val Leu Ile Cys
145 150 155 160

Phe Gly Lys Glu Ala Val Asp Leu Ala Val Ala His Asn Ser Asp Phe
165 170 175

Lys Leu Pro Cys Glu Val Arg Gly Ser Thr Phe Asp Val Val Thr Leu
180 185 190

Leu Lys Ser Arg Asp Pro Thr Ser Glu Asp Lys His Trp Phe Tyr Val
195 200 205

Ala Ala Thr Arg His Arg Ser Lys Leu Ile Ile Met Gln
210 215 220

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ATGCCTTTTC AGCAACCTGC CAACTGGGCT AAGACCATAA CTCCATTAAC TATTGGTTTG 60
GGCATTGGGT TGGTTCTGCA CTTCTTAAGG AAATCAAATC TGCCATATTC AGGAGACAAT 120
ATTCACCAGT TCCCACACGG AGGGCATTAC AGGGACGGCA CGAAGAGTAT AACCTATTGT 180
GGCCCTAGGC AGTCATTCCC AAGCTCAGGA ATATTCGGTC AGTCTGAAAA TTTCGTACCT 240
CTAATATTGG TCGTGACTCT GGTCGCTTTT ATACATGCGT TATCTCTTG GAATTCTGGT 300
CCTAGTAGGA GTTGCAATTG CCATCCAAAT CCTTGCACAT GTAGACAGCA GTAG 354

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 117 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met	Pro	Phe	Gln	Gln	Pro	Ala	Asn	Trp	Ala	Lys	Thr	Ile	Thr	Pro	Leu
1					5					10					15
Thr	Ile	Gly	Leu	Gly	Ile	Gly	Leu	Val	Leu	His	Phe	Leu	Arg	Lys	Ser
					20				25				30		
Asn	Leu	Pro	Tyr	Ser	Gly	Asp	Asn	Ile	His	Gln	Phe	Pro	His	Gly	Gly
						35		40				45			
His	Tyr	Arg	Asp	Gly	Thr	Lys	Ser	Ile	Thr	Tyr	Cys	Gly	Pro	Arg	Gln
						50		55		60					
Ser	Phe	Pro	Ser	Ser	Gly	Ile	Phe	Gly	Gln	Ser	Glu	Asn	Phe	Val	Pro
						65		70		75			80		
Leu	Ile	Leu	Val	Val	Thr	Leu	Val	Ala	Phe	Ile	His	Ala	Leu	Ser	Leu
						85			90			95			
Trp	Asn	Ser	Gly	Pro	Ser	Arg	Ser	Cys	Asn	Cys	His	Pro	Asn	Pro	Cys
						100		105			110				
Thr	Cys	Arg	Gln	Gln											
					115										

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 243 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ATGCGTTATC	TCTTTGGAAT	TCTGGTCCTA	GTAGGAGTTG	CAATTGCCAT	CCAAATCCTT	60
GCACATGTAG	ACAGCAGTAG	TGGCAACCAT	CAAGGCTGTT	TCATAAGAGC	CACCGGGGAG	120
TCAAATAGTAA	TTGAGAATTG	TGGGCCGAGC	GAGGCCCTAG	CTGCTACAGT	CAAAGAGGTG	180

TTGGGCGGTC TAAAGGCTTT AGGGGTTAGC CAAAAGGTTG ATGAAATTAA TTACAGTTGT	240
TGA	243

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 80 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met Arg Tyr Leu Phe Gly Ile Leu Val Leu Val Gly Val Ala Ile Ala			
1	5	10	15
Ile Gln Ile Leu Ala His Val Asp Ser Ser Ser Gly Asn His Gln Gly			
20	25	30	
Cys Phe Ile Arg Ala Thr Gly Glu Ser Ile Val Ile Glu Asn Cys Gly			
35	40	45	
Pro Ser Glu Ala Leu Ala Ala Thr Val Lys Glu Val Leu Gly Gly Leu			
50	55	60	
Lys Ala Leu Gly Val Ser Gln Lys Val Asp Glu Ile Asn Tyr Ser Cys			
65	70	75	80

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 631 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ATGGCAAGTC AAGTTGGAAA ATTGCCTGGC GAATCAAATG AAGCATATGA GGCTAGACTC	60
AAGGCTTTAG AGTTAGCAAG GGCCCAAAAA GCTCCAGAAG TCTCCAACCA ACCTCCCACA	120
CTTGGAGGCA TTCTAGCCAA AAGGAAAAGA GTGATTGAGA ATGCACCTCTC AAAGACAGTG	180
GATATGCGTG AAGTCTTAAG GCATGAATCT GTTGTACTCT CCCCGAATGT AATGGACGAG	240
GGAGCAATAG ACGAGCTGAT TCGTGCCTTT GGGGAGTCGG GCATAGCTGA AAATGTGCAG	300

TTTGATGTTG CAATAGACAT TGCTGCCAC TGTTCTGATG TGGGGAGCTC TCAGAGGTCA	360
ACCCCTTATTG GTAAAAGCCC CTTCTGTGAG TTAAATAGGT CTGAAATTGC CGGAATAATA	420
AGGGAGGTGA CCACGCTGCG CAGATTTGC ATGTACTACG CAAAGATTGT GTGGAACATC	480
CATTTGGAGA CGGGAATACC ACCAGCTAAT TGGGCCAAGA AAGGATTAA TGAGAATGAA	540
AAGTTTGCAG CCTTGACTT CTTCTTGGA GTCACAGATG AAAGCGCGCT TGAGCCTAAG	600
GGTGGAGTCA AGAGAGCTCC AACAAAAGCA G	631

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 210 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Met Ala Ser Gln Val	5	Gly Lys Leu Pro	10	Gly Glu Ser Asn	Glu Ala Tyr
1					15
Glu Ala Arg Leu Lys	20	Ala Leu Glu	25	Leu Ala Arg Ala Gln	Lys Ala Pro
					30
Glu Val Ser Asn Gln Pro	35	Pro Thr Leu Gly	40	Gly Ile Leu Ala Lys	Arg
					45
Lys Arg Val Ile Glu Asn	50	Ala Leu Ser Lys	55	Thr Val Asp Met	Arg Glu
					60
Val Leu Arg His Glu Ser	65	Val Val Leu Ser	70	Pro Asn Val Met Asp	Glu
					80
Gly Ala Ile Asp Glu Leu Ile Arg	85	Ala Phe Gly	90	Glu Ser Gly Ile Ala	
					95
Glu Asn Val Gln Phe Asp Val	100	Ala Ile Asp Ile Ala Arg	105	His Cys Ser	
					110
Asp Val Gly Ser Ser Gln Arg	115	Ser Thr Leu Ile Gly	120	Lys Ser Pro Phe	
					125
Cys Glu Leu Asn Arg Ser	130	Glu Ile Ala Gly	135	Ile Arg Glu Val	Thr
					140
Thr Leu Arg Arg Phe Cys Met	145	Tyr Tyr Ala Lys	150	Ile Val Trp Asn	Ile
					160
His Leu Glu Thr Gly Ile Pro	165	Pro Ala Asn Trp	170	Ala Lys Lys Gly	Phe
					175

Asn Glu Asn Glu Lys Phe Ala Ala Phe Asp Phe Phe Leu Gly Val Thr
180 185 190

Asp Glu Ser Ala Leu Glu Pro Lys Gly Gly Val Lys Arg Ala Pro Thr
195 200 205

Lys Ala
210

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2009 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GAAGCTAGCA CATTCTGTT CAACACTATG GCTAACATGT TGTCACATT TCTGAGATAT	60
GAACTGACGG GTTCAGAGTC AATAGCATT GCAGGGGATG ATATGTGTGC TAATAGAAGG	120
TTGCGGCTTA AAACGGAGCA TGAGGGTTTT CTGAACATGA TCTGCCTTAA GGCCAAGGTT	180
CAGTTTGTAA CCAACCCCCAC ATTCTGTGGA TGGTGCTTAT TTAAGGAGGG AATCTTCAAG	240
AAACCTCAAC TAATTTGGGA GCGAATATGC ATAGCCAGAG AGATGGGCAA TCTGGAGAAC	300
TGTATTGACA ATTATGCGAT AGAAAGTGTCC TATGCATATA GATTGGGTGA GCTATCAATT	360
GAAATGATGA CAGAAGAAGA AGTGGAGGCA CACTACAATT GTGTGAGGTT CCTGGTTAGG	420
AACAAGCATA AGATGAGGTG CTCATTCA GGCTGTTTG AAGTGGTTGA TTAGGCCTTA	480
AGTATTGAGC GTTGTTCGAG TTATTATGAA TAATTTAGTT AAAGCATTAT CAGCCTTCGA	540
GTTCATAGGT GTTTCAATG TGCTCAAATT TCCAGTTGTT ATACATAGTG TGCCTGGTAG	600
TGGTAAGAGT AGCTTAATAA GGGATTAAAT CTCAGAGGAC GAGAGTTTCG TGGCTTTCAC	660
AGCAGGTGTT CCAGACAGTC CTAACCTCAC AGGGAGGTAC ATCAAGCCTT ACTCACCAGG	720
ATGCGCAGTG CAAGGAAAAG TGAATATACT TGATGAGTAC TTGTCCGTT AAGACATTTC	780
GGGTTTGAT GTACTGTTT CAGACCCGTA CCAGAAATATC AGTATTCCCC AAGAGGCGCA	840
TTTCATTAAG TCCAAGACTT GTAGGTTGG TGTGAACACT TGCAAATACC TTTCCTCTTT	900
CGGTTTCGAA GTTAGCAGCG ACGGGCTGGA CGACGTCATT GTGGGATCGC CCTTCACTCT	960
AGATGTTGAA GGGGTGCTGA TATGTTTGG CAAGGAGGCG GTAGATCTCG CTGTTGCGCA	1020
CAAATCTGAA TTCAAGTTGC CGTGTGAGGT TCGAGGTTCA ACCTCAATG TGGTAACCCCT	1080

TTTGAAATCA AGAGACCAA CCCCAGAGGA CAGGCAGTGG TTTTACATCG CTGCCACAAG	1140
ACATAGGAAG AAATTGGTCA TTATGCAGTA AAATGCCTT TCAGCAGCCT GCTAATTGGG	1200
CAAAAACCAT AACTCCATTG ACTATTGGCT TAGGAATTGG ACTTGTGCTG CATTTCCTGA	1260
GAAAGTCAAA TCTACCATAT TCAGGAGACA ACATCCATCA ATTCCTCAC GGGGGGCGTT	1320
ACCGGGACGG CACAAAAAGT ATAACTTACT GTGGCCCTAA GCAGTCCTTC CCCAGTTCAG	1380
GAATATTTGG TCAGTCTGAG AATTTGTGC CCTTAATGCT TGTCTAGGT CTAATTGCAT	1440
TCATACATGT ATTGTCTGTT TGGAATTCTG GTCTTGGTAG GAATTGCAAT TGCCATCCAA	1500
ATCCTTGCTC ATGTAGACAA CAGTAGTGGC AGTCACCAAG GTTGCTTTAT CAGGGCCACT	1560
GGAGAGTCTA TTTTGATTGA AAATTGTGGC CCAAGCGAGG CCCTTGCATC AACAGTGAGG	1620
GAGGTGTTGG GGGGTTGAA GGCTTTAGGA ATTAGCCATA CTACTGAAGA AATTGATTAT	1680
CGTTGTTAAA TTGGTTAAAT GGCGAGTCAA GTTGGTAAGC TCCCCGGAGA ATCAAATGAG	1740
GCATTTGAAG CCCGGCTGAA ATCACTGGAG TTGGCTAGAG CTCAAAAGCA GCCAGAAGGT	1800
TCAAACACAC CGCCTACTCT CAGTGGTGTG CTTGCCAAC GTAAGAGGGT TATTGAGAAT	1860
GCACTCTCAA AGACAGTGGA CATGAGGGAG GTGTTGAAAC ACGAAACGGT TGTAAATTCC	1920
CCAAATGTCA TGGATGAGGG TGCAATAGAT GAACTGATTG GTGCATTGG AGAATCAGGC	1980
ATAGCTGAGA GCGCACATT TGATGTGGC	2009

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 447 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GAAGCTAGCA CATTCTGTT CAACACTATG GCTAACATGT TGTCACCTT TCTGAGATAT	60
GAACTGACGG GTTCAGAGTC AATAGCATT GCAGGGATG ATATGTGTGC TAATAGAAGG	120
TTGCGGCTTA AAACGGAGCA TGAGGGTTT CTGAACATGA TCTGCCTTAA GGCCAAGGTT	180
CAGTTGTTT CCAACCCAC ATTCTGTGGA TGGTGCTTAT TTAAGGAGGG AATCTCAAG	240
AAACCTCAAC TAATTGGGA GCGAATATGC ATAGCCAGAG AGATGGGCAA TCTGGAGAAC	300
TGTATTGACA ATTATGCGAT AGAAGTGTCC TATGCATATA GATTGGGTGA GCTATCAATT	360
GAAATGATGA CAGAAGAAGA AGTGGAGGCA CACTACAATT GTGTGAGGTT CCTGGTTAGG	420

AACAAGCATA AGATGAGGTG CTCATT

447

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 149 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Glu	Ala	Ser	Thr	Phe	Leu	Phe	Asn	Thr	Met	Ala	Asn	Met	Leu	Phe	Thr
1					5				10					15	
Phe	Leu	Arg	Tyr	Glu	Leu	Thr	Gly	Ser	Glu	Ser	Ile	Ala	Phe	Ala	Gly
			20					25					30		
Asp	Asp	Met	Cys	Ala	Asn	Arg	Arg	Leu	Arg	Leu	Lys	Thr	Glu	His	Glu
			35					40				45			
Gly	Phe	Leu	Asn	Met	Ile	Cys	Leu	Lys	Ala	Lys	Val	Gln	Phe	Val	Ser
			50				55				60				
Asn	Pro	Thr	Phe	Cys	Gly	Trp	Cys	Leu	Phe	Lys	Glu	Gly	Ile	Phe	Lys
			65			70			75				80		
Lys	Pro	Gln	Leu	Ile	Trp	Glu	Arg	Ile	Cys	Ile	Ala	Arg	Glu	Met	Gly
					85		90						95		
Asn	Leu	Glu	Asn	Cys	Ile	Asp	Asn	Tyr	Ala	Ile	Glu	Val	Ser	Tyr	Ala
					100				105				110		
Tyr	Arg	Leu	Gly	Glu	Leu	Ser	Ile	Glu	Met	Met	Thr	Glu	Glu	Glu	Val
					115			120				125			
Glu	Ala	His	Tyr	Asn	Cys	Val	Arg	Phe	Leu	Val	Arg	Asn	Lys	His	Lys
					130			135				140			
Met	Arg	Cys	Ser	Ile											
				145											

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 666 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

ATGAATAATT TAGTTAAAGC ATTATCAGCC TTCAAGTTA TAGGTGTTT CAATGTGCTC	60
AAATTTCCAG TTGTTATACA TAGTGTGCCT GGTAGTGGTA AGAGTAGCTT AATAAGGGAA	120
TTAACATCTAG AGGACGAGAG TTTCGTGGCT TTCACAGCAG GTGTTCCAGA CAGTCCTAAC	180
CTCACAGGGA GGTACATCAA GCCTTACTCA CCAGGATGCG CAGTGCAAGG AAAAGTGAAT	240
ATACTTGATG AGTACTTGTC CGTTCAAGAC ATTCGGGTT TTGATGTACT GTTTTCAGAC	300
CCGTACCAGA ATATCAGTAT TCCCCAAGAG GCGCATTCA TTAAGTCAA GACTTGTAGG	360
TTTGGTGTGA ACACTTGCAA ATACCTTCC TCTTCGGTT TCGAAGTTAG CAGCGACGGG	420
CTGGACGACG TCATTGTGGG ATCGCCCTTC ACTCTAGATG TTGAAGGGGT GCTGATATGT	480
TTTGGCAAGG AGGCGGTAGA TCTCGCTGTT GCGCACAACT CTGAATTCAA GTTGCCGTGT	540
GAGGTTCGAG GTTCAACCTT CAATGTGGTA ACCCTTTGA AATCAAGAGA CCCAACCCCA	600
GAGGACAGGC ACTGGTTTA CATCGCTGCC ACAAGACATA GGAAGAAATT GGTCATTATG	660
CAGTAA	666

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 221 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Met Asn Asn Leu Val Lys Ala Leu Ser Ala Phe Glu Phe Ile Gly Val			
1	5	10	15
Phe Asn Val Leu Lys Phe Pro Val Val Ile His Ser Val Pro Gly Ser			
20	25	30	
Gly Lys Ser Ser Leu Ile Arg Glu Leu Ile Ser Glu Asp Glu Ser Phe			
35	40	45	
Val Ala Phe Thr Ala Gly Val Pro Asp Ser Pro Asn Leu Thr Gly Arg			
50	55	60	
Tyr Ile Lys Pro Tyr Ser Pro Gly Cys Ala Val Gln Gly Lys Val Asn			
65	70	75	80
Ile Leu Asp Glu Tyr Leu Ser Val Gln Asp Ile Ser Gly Phe Asp Val			
85	90	95	

Leu Phe Ser Asp Pro Tyr Gln Asn Ile Ser Ile Pro Gln Glu Ala His
100 105 110

Phe Ile Lys Ser Lys Thr Cys Arg Phe Gly Val Asn Thr Cys Lys Tyr
115 120 125

Leu Ser Ser Phe Gly Phe Glu Val Ser Ser Asp Gly Leu Asp Asp Val
130 135 140

Ile Val Gly Ser Pro Phe Thr Leu Asp Val Glu Gly Val Leu Ile Cys
145 150 155 160

Phe Gly Lys Glu Ala Val Asp Leu Ala Val Ala His Asn Ser Glu Phe
165 170 175

Lys Leu Pro Cys Glu Val Arg Gly Ser Thr Phe Asn Val Val Thr Leu
180 185 190

Leu Lys Ser Arg Asp Pro Thr Pro Glu Asp Arg His Trp Phe Tyr Ile
195 200 205

Ala Ala Thr Arg His Arg Lys Lys Leu Val Ile Met Gln
210 215 220

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 354 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

ATGCCTTTC AGCAGCCTGC TAATTGGCA AAAACCATAA CTCCATTGAC TATTGGCTTA 60
GGAATTGGAC TTGTGCTGCA TTTTCTGAGA AAGTCAAATC TACCATATTC AGGAGACAAC 120
ATCCATCAAAT TTCCCTCACGG GGGGCGTTAC CGGGACGGCA CAAAAAGTAT AACTTACTGT 180
GGCCCTAACGC AGTCCTTCCC CAGTTCAGGA ATATTTGGTC AGTCTGAGAA TTTTGTCGCC 240
TTAATGCTTG TCATAGGTCT AATTGCATTG ATACATGTAT TGTCTGTTG GAATTCTGGT 300
CTTGGTAGGA ATTGCAATTG CCATCCAAAT CCTTGCTCAT GTAGACAAACA GTAG 354

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 116 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met Pro Phe Gln Gln Pro Ala Asn Trp Ala Lys Thr Ile Thr Pro Leu
1 5 10 15

Thr Ile Gly Leu Gly Ile Gly Leu Val Leu His Phe Leu Arg Lys Ser
20 25 30

Asn Leu Pro Tyr Ser Gly Asp Asn Ile His Gln Phe Pro His Gly Gly
35 40 45

Arg Tyr Arg Asp Gly Thr Lys Ile Thr Tyr Cys Gly Pro Lys Gln Ser
50 55 60

Phe Pro Ser Ser Gly Ile Phe Gly Gln Ser Glu Asn Phe Val Pro Leu
65 70 75 80

Met Leu Val Ile Gly Leu Ile Ala Phe Ile His Val Leu Ser Val Trp
85 90 95

Asn Ser Gly Leu Gly Arg Asn Cys Asn Cys His Pro Asn Pro Cys Ser
100 105 110

Cys Arg Gln Gln
115

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

ATGTATTGTC TGTTTGAAT TCTGGTCTTG GTAGGAATTG CAATTGCCAT CCAAATCCTT 60
GCTCATGTAG ACAACAGTAG TGGCAGTCAC CAAGGTTGCT TTATCAGGGC CACTGGAGAG 120
TCTATTTGA TTGAAAATTG TGGCCCAAGC GAGGCCCTTG CATCAACAGT GAGGGAGGTG 180
TTGGGGGGTT TGAAGGCTTT AGGAATTAGC CATACTACTG AAGAAATTGA TTATCGTTGT 240
TAA 243

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Met Tyr Cys Leu Phe Gly Ile Leu Val Leu Val Gly Ile Ala Ile Ala
1 5 10 15

Ile Gln Ile Leu Ala His Val Asp Asn Ser Ser Gly Ser His Gln Gly
20 25 30

Cys Phe Ile Arg Ala Thr Gly Glu Ser Ile Leu Ile Glu Asn Cys Gly
35 40 45

Pro Ser Glu Ala Leu Ala Ser Thr Val Arg Glu Val Leu Gly Gly Leu
50 55 60

Lys Ala Leu Gly Ile Ser His Thr Thr Glu Glu Ile Asp Tyr Arg Cys
65 70 75 80

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 311 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

ATGGCGAGTC AAGTTGGTAA GCTCCCCGGA GAATCAAATG AGGCATTGAG AGCCCGGCTG 60
AAATCACTGG AGTTGGCTAG AGCTAAAAG CAGCCAGAAG GTTCAAACAC ACCGCCTACT 120
CTCAGTGGTG TGCTTGCCAA ACGTAAGAGG GTTATTGAGA ATGCACTCTC AAAGACAGTG 180
GACATGAGGG AGGTGTTGAA ACACGAAACG GTTGTAAATT CCCCAAATGT CATGGATGAG 240
GGTGCAATAG ATGAACTGAT TCGTGCATTC GGAGAACATAG GCATAGCTGA GAGCGCACAA 300
TTTGATGTGG C 311

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 103 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Met Ala Ser Gln Val Gly Lys Leu Pro Gly Glu Ser Asn Glu Ala Phe
1 5 10 15

Glu Ala Arg Leu Lys Ser Leu Glu Leu Ala Arg Ala Gln Lys Gln Pro
20 25 30

Glu Gly Ser Asn Thr Pro Pro Thr Leu Ser Gly Val Leu Ala Lys Arg
35 40 45

Lys Arg Val Ile Glu Asn Ala Leu Ser Lys Thr Val Asp Met Arg Glu
50 55 60

Val Leu Lys His Glu Thr Val Val Ile Ser Pro Asn Val Met Asp Glu
65 70 75 80

Gly Ala Ile Asp Glu Leu Ile Arg Ala Phe Gly Glu Ser Gly Ile Ala
85 90 95

Glu Ser Ala Gln Phe Asp Val
100

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1206 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GCAGGATTGA AGGCTGGCCA CTGTGTGATT TTTGATGAGG TCCAGTTGTT TCCTCCTGGA 60
TACATCGATC TATGCTTGCT TATTATACGT AGTGATGCTT TCATTTCACT TGCCGGTGAT 120
CCATGTCAA GCACATATGA TTTCGAAAAG GATCGGGCAA TTTTGGGCGC TGAGCAGAGT 180
GACATACTTA GAATGCTTGA GGGCAAAACG TATAGGTATA ACATAGAAAG CAGGAGGTTT 240
GTGAACCAA TGTCGAATC AAGACTGCCA TGTCACTTCA AAAAGGGTTC GATGACTGCC 300
GCTTTCGCTG ATTATGCAAT CTTCCATAAT ATGCATGACT TTCTCCTGGC GAGGTCAAAA 360
GGTCCTTGG ATGCCGTTTT GGTTCCAGT TTTGAGGAGA AAAAGATAGT CCAGTCCTAC 420
TTTGGAAATGA AACAGCTCAC ACTCACATT GGTGAATCAA CTGGGTTGAA TTTCAAAAAT 480

GGGGGAATTC TCATATCACA TGATTCCTTT CACACAGATG ATCGGCCGGT GGCTTACTGC	540
TTTATCTCGC TTCAGCCACA ATTTGGATT GGTGAACATT ACAGGTCTGA GGGTGGAAAG	600
TTTCCTCTCG CACTTGCTG GCAAACCCCT CTACCATT TTAAACAGCCA AAAGTGGGA	660
GAATGTCATA CGAGATTGTC TCCCAGGTGA GCCTAACCTTC TTCAGTGGCT TTAACGTTAG	720
CATTGGAAAG AATGAAGGTG TTAGGGAGGA GAAGTTATGT GGTGACCCAT GGTTAAAAGT	780
CATGCTTTTC CTGGGTCAAG ATGAGGATTG TGAAGTTGAA GAGATGGAGT CAGAGTGCTC	840
AAATGAAGAA TGGTTAAAA CCCACATTCC CCTGAGTAAT CTGGAGTCAA CCAGGGCTAG	900
GTGGGTGGGT AAAATGGCTT TGAAAGAGTA TCAGGGAGGTG CGTTGTGGTT ATGAAATGAC	960
TCAACAATTTC TTTGATGAGC ATAGGGTGG AACTGGTGAG CAACTGAGCA ATGCATGTGA	1020
GAGGTTTGAA AGCATTACCA CAAGGCATAA AGGAAATGAT TCAATAACCT TCCTTATGGC	1080
TGTCCGAAAG CGTCTCAAAT TTTCGAAGCC CCAGGTTGAA GCTGCCAAC TGAGGCGGGC	1140
CAAACCATAT GGGAAATTCT TATTAGACTT TCCTATCCAA AATCCCATTG AAAGCCAGTC	1200
ATAATT	1206

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1284 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

ATTAACCCAA ATGGTAAGAT TTCCGCCTTG TTTGATATAA CCAATGAGCA CATAAGGCAT	60
GTTGAGAAGA TCGGCAATGG CCCTCAGAGC ATAAAAAGTAG ATGAGTTGAG GAAGGTTAAG	120
CGATCCGCCCT TTGATCTTCT TTCAATGAAT GGGTCCAAAA TAACCTATTT TCCAAACTTT	180
GAGCGGGCTG AAAAGTTGCA AGGGTGCTTG CTAGGGGGCC TAACTGGTGT CATAAGTGAT	240
GAAAAGTTCA GTGATGCAAA ACCCTGGCTT TCTGGTATAT CAACTGCGGA TATAAAGCCA	300
AGAGAGCTAA CTGTCGTGCT TGGCACTTTT GGGGCTGGAA AGAGTTTCTT GTATAAGAGT	360
TTCATGAAGA GATCTGAGGG AAAATTGTA ACTTTGTTT CCCCTAGACG AGCCTTGGCA	420
AATTCAATCA AAAATGATCT TGAAATGGAT GATGGCTGCA AAGTTGCCAA AGCAGGCAAA	480
TCAAAGAAGG AAGGGTGGGA TGTAGTGACC TTTGAAGTTT TCCTTAGAAA AGTTTCTGGT	540
TTGAAAGCTG GTCATTGTGT GATTTTGAT GAGGTTCACT TGTTCCCCC TGGATAACATC	600

GATCTGTGTT TACTTGTCA	ACGAAGTGAT GCTTCATTT CACTTGCTGG TGATCCATGC	660
CAGAGCACAT ATGATTACA	GAAGGATCGA GCAATTTGG GAGCTGAGCA GAGTGACATA	720
CTCAGACTGC TTGAAGGAAA	GACATATAGG TACAACATAG AAAGCAGACG TTTTGTGAAC	780
CCAATGTTG AATCTAGACT	ACCATGTCAC TTCAAAAAGG GTTCAATGAC TGCGAGCCTT	840
GCTGATTATG CAATCTCCA	CAATATGCAT GACTTCCTCC TGGCGAGGTC AAAAGGCC	900
TTGGATGCTG TTCTAGTTTC	CAGTTTGAG GAGAAGAAAA TAGTCCAATC CTACTTTGGG	960
ATGAAGCAAC TCACTCTCAC	ATTTGGTGAA TCAACTGGGT TGAACCTCAA AAATGGAGGA	1020
ATTCTCATAT CACATGACTC	CTTCATACT GACGATCGAC GGTGGCTTAC TGCTTTATCT	1080
CGATTCAAGCC ATAATTTGGA	TTTGGTGAA ACATCACAGGTC TTGAGGGTGG AAAGTTTCT	1140
CTCACATTG GCTGGTAAAC	CCCTTTACCA CTTTTGACG GCTTAAAAGT GGAGAGAATG	1200
TCATACGAGA CCTGCTTCAG	GTGAGCCTAA CTTCTTTAG GGGTTCAATG TCAGCATTGG	1260
AAAAAAATGG AAGGGGTTAG AGAA		1284

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1402 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CATTTTTAAA ATTTAATCCA	GTCGACTCAC CAAATGTGAG CGTAAGCTGT TTCATCCCAA	60
AGTAGGACTG GACTATTTTC	TTCTCCTCAA AACTAGAAC CAGAATGGCA TCCAAAGGAC	120
CTTTTGACCT TGCCAGGAGG	AAATCATGCA TATTGTGGAA AATGGCATAA TCAGCAAAGG	180
CAGCAGTCAT TGTACCCCTT	TTGAAGTGAC ATGGCAGTCG AGATTCAAAC ATTGGGTTCA	240
CAAATCTTCT GCTTCTATG	TTGTACCTAT ACGTCTTGCC TTCAAGTATT TTGAGTATGT	300
CACTCTGCTC AGCGCCAAA	ATCGCCCGAT CTTTTGTGA GTCATATGTG CTCTGACATG	360
GGTCACCAGC AAGTGAAATG	AAAGCATCAC TACGTATAAT AAGCAAACAT AGATCGATGT	420
ATCCAGGGGG AAACAACCTGG	ACCTCATCGA AAATTACACA GTGACCAGCT TTTAGACCTG	480
CAACTTTCT AAGGAAGACT	TCAAAAGTCA CAACATCCCA TCCTTCCTTC TTTGACCTGC	540
CTGCTTGGC AACTTTGCAG	CTATCATCCA TTTCAAGATC ATTTTGATT GAATTGCTA	600

GAGCCCGTCT	GGGGGAAACA	AAAGTTACGA	ATTTACCCCTC	AGATCTTTTC	ATAAAGCTCT	660
TGTACAAAAA	GCTTTTCCG	GCTCCAAATG	TGCCAAGCAC	AACAGTTAGC	TCCCTCGGCT	720
TAATGTCAGT	AGTTGATATA	CCAGAAAGCC	AGGGCTTG	ATCACTGAAC	TTCTCATCAC	780
TTATGACACC	AGTTAGGCCT	CCTAGCAGAC	ACCCCTGCAA	CTTTTCAGCC	CGCTCAAAAC	840
TTGGGAAGTA	GGTTACCTG	GACCCATTAA	TTGAAAGAAG	ATCAAGGGCG	GATCGCTTGA	900
CCTTCGCAA	TTCATCTACT	TTAATGCTCT	GAGGGCCATT	ACCTATCTT	TCAACATGCC	960
TTATGTGCTC	ATTAGTTATG	TCAAACAGAG	CGGAAAACCTT	GCCATGTGG	TTAATCACCT	1020
CAATTTCCCC	ATTTATGTCA	CACTTAGCGC	AAATGTCAA	AGCCTCAAAG	GCTTCAGCTA	1080
AGTTACATCA	TGTTGAGCCT	CCCCCTGGC	AAAGCTCCTC	AAAAATGTGG	TTAGTGCTAG	1140
TGCAACCATC	CATGGGGCAC	ATGGTTGAA	TTGATTGATT	TAAGGCAAAA	ATCCCCACAG	1260
GGGGCATCCC	CTTCCCCAAT	TTCCACTGAT	TCATACTCTG	GCGTTATCAT	ATCAACCCAA	1320
TGTGTCAAAT	ACAAATAATG	CAATCTCTA	TCTCCGATAA	CATTTCCCCC	ATTTTTAAA	1380
AATGGTGGGG	TGAAAATTGG	AA				1402

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1236 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GTGGTTTTG	CAACAACAGG	CCCAGGTCTA	TCTAAGGTTT	TGGAAATGCC	TCGAAGCAAG	60
AAGCAATCTA	TTCTGGTTCT	TGAGGGAGCC	CTATCCATAG	AAACGGACTA	TGGCCCAAAA	120
GTTCTGGGAT	CTTTGAAGT	TTTCAAAGGG	GATTCAACA	TTAAAAAAAT	GGAAGAAAGT	180
TCCATCTTG	TAATAACATA	CAAGGCCCA	GTTAGATCTA	CTGGCAAGTT	GAGGGTCCAC	240
CAATCAGAAT	GCTCATTTC	TGGATCCAAG	GAGGTATTGC	TGGGTTGTCA	GATTGAGGCA	300
TGTGCTGATT	ATGATATTGA	TGATTTCAAT	ACTTTCTTG	TACCTGGTGA	TGGTAATTGC	360
TTTTGGCATT	CAGTTGGTTT	CTTACTCAGT	ACTGACGGAC	TTGCTTGAA	GGCCGGCATT	420
CGTTCTTCG	TGGAGAGTGA	ACGCCTGGTG	AGTCCAGATC	TTTCAGCCCC	AACCATTCT	480
AAACAACTGG	GGGAAAATGC	TTATGCCGAG	AATGAGATGA	TTGCATTATT	TTGTATTGCA	540

CACCATGTGA GGCTGATAGT GATTACGCCA GAGTATGAAG TCAGTTGGAA ATTTGGGGAA	600
GGTGAATGGC CCCTGTGCGG AATTCTTCGC CTTAAATCAA ATCACTTCCA ACCATGTGCC	660
CCATTGAATG GTTGCATGAT TACAGCTATT GCTTCAGCAC TTGGTAGGCG TGAAGTTGAT	720
GTGCTTAATT ATCTGTGCAG GCCTAGCACT AACCCACATTT TTGAGGAGCT TTGCCAAGGG	780
GGAGGCCTCA ACATGATGTA CTTAGCTGAA GCCTTGAGG CTTTGACAT TTGCGCTAAC	840
TGTGACATAA ATGGGGAAAT TGAGGTGATT AATCCACATG GCAAGTTTC CGCTCTGTT	900
GACATAACTA ATGAGCACAT AAGGCATGTT GAAAAGATAG GTAATGGCCC TCAGAGCATT	960
AAAGTAGATG AATTGCGAAA GGTCAAGCGA TCTGCCCTTG ATCTTCTTTC AATTAATGGG	1020
TCCAAGGTAA CCTACTTCCC AAGTTTGAG CGGGCTGAAA AGTTGCAAGG GTGTCTGCTA	1080
GGAGGCCTAA CTGGTGTCA AAGTGTGAG AAAGTCAGTG ATGCAAAGCC CTGCTTTTG	1140
GTATATCAAC TACTGACATT AAGCCGAGGG AGCTAACTGT TGTGCTTTGG CACATTTGGA	1200
GCCCCGGAAAA AGCCTTTGT ACCAAGAGCT TTATTG	1236

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1296 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GTCTAACTGG CGTTATAAGT GATGAGAAAT TCAGTGATGC AAAACCTTGG CTTTCTGGTA	60
TATCTACTAC AGATATTAAG CCAAGGGAAT TAACTGTTGT GCTTGGTACA TTTGGGGCTG	120
GGAAGAGTTT CTTGTACAAG AGTTTCATGA AAAGGTCTGA GGGTAAATTC GTAACCTTG	180
TTTCTCCAG ACGTGCTTTA GCAAATTCAA TCAAAATGA TCTTGAAATG GATGATAGCT	240
GCAAAGTTGC CAAAGCAGGT AGGTCAAAGA AGGAAGGGTG GGATGTAGTA ACTTTGAGG	300
TCTTCCTCAG AAAAGTTGCA GGATTGAAGG CTGGCCACTG TGTGATTTT GATGAGGTCC	360
AGTTGTTCC TCCTGGATAC ATCGATCTAT GCTTGCTTAT TATACGTAGT GATGCTTCA	420
TTTCACTTGC CGGTGATCCA TGTCAAAGCA CATATGATTC GCAAAAGGAT CGGGCAATT	480
TGGGCGCTGA GCAGAGTGAC ATACTTAGAA TGCTTGAGGG CAAAACGTAT AGGTATAACA	540
TAGAAAGCAG GAGGTTTGTG AACCCAATGT TCGAATCAAG ACTGCCATGT CACTTCAAAA	600

AGGGTTCGAT GACTGCCGCT TTGCGCTGATT ATGCAATCTT CCATAATATG CATGACTTTC	660
TCCTGGCGAG GTCAAAAGGT CCTTTGGATG CCGTTTGTT TTCCAGTTT GAGGAGAAAA	720
AGATAGTCCA GTCCTACTTT GGAATGAAAC AGCTCACACT CACATTGGT GAATCAACTG	780
GGTTGAATT CAAAAATGGG GGAATTCTCA TATCACATGA TTCCCTTCAC ACAGATGATC	840
GGCGGTGGCT TACTGCTTA TCTCGCTTCA GCCACAATT GGATTGGTG AACATTACAG	900
GTCTGAGGTG GAAAGTTCC TCTCGCAGTT TGCTGGCAA CCCCTCTACC ATTTTTAAC	960
AGCCAAAAGT GGGGAGAATG TCATACGAGA TTTGCTCCC GGTGAGCCTA ACTTCTTCAG	1020
TGGCTTAAAC GTTAGCATTG GAAAGAATGA AGGTGTTAGG GAGGAGAAGT TATGTGGTGA	1080
CCCATGGTTA AAAGTCATGC TTTTCCTGGG TCAAGATGAG GATTGTGAAG TTGAAGAGAT	1140
GGAGTCAGAG TGCTCAAATG AAGAATGGTT TAAAACCCAC ATTCCCCTGA GTAATCTGGA	1200
GTCAACCAGG GCTAGGTGGG TGGGTAAAAT GGCCTTGAAA GAGTATCGGG AGGTGCGTTG	1260
TGGTTATGAA ATGACTCAAC AATTCTTGA TGACAT	1296

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 907 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

ATGTTCACCA AATCCAAATT ATGGCTGAAG CGAGATAAAG CAGTAAGCCA CCGCCGATCA	60
TCTGTGTGAA AGGAATCATG TGATATGAGA ATTCCCCAT TTTGAAATT CAACCCAGTT	120
GATTCAACCA ATGTGAGTGT GAGCTGTTTC ATTCCAAAGT AGGACTGGAC TATCTTTTC	180
TCCTCAAAAC TGGAAACCAA AACGGCATCC AAAGGACCTT TTGACCTCGC CAGGAGAAAG	240
TCATGCATAT TATGGAAGAT TGCATAATCA GCGAAAGCGG CAGTCATTGA GCCCTTTTG	300
AATTGACATG GCAGTCTTGA TTCGAACATT GGATTCAACAA ACCTCCTGCT TTCAATGTTA	360
TACCTATACG TCTGCCCTC AAGCAGTCTA AGTATGTCAC TCTGCTCAGC GCCCAAAATT	420
GCCCGATCCT TTTGCGAATC ATATGTGCTT TGACATGGAT CACCGGCAAG TGAAATGAAA	480
GCATCACTAC GTATAATAAG CAAGCATAGA TCGATGTATC CAGGAGGAAA CAACTGGACC	540
TCATCGAAAA TCACACAGTG GCCAGCCTTC AATCCTGCAA CTTTCTGAG GAAAACCTCA	600
AAAGTTACTA CATCCCACCC TTCCCTCTTT GACCTACCTG CTTAGCAAC TTGCGAGCTA	660

TCATCCATT CAAGATCATT TTTGATTGAA TTTGCTAAAG CACGTCTGGG AGAAACAAAG	720
GTTACGAATT TACCCCTCAGA CCTTTTCATG AAACCTTGT ACAAGAAACT CTTCCCAGCC	780
CCAAATGTAC CAAGCACGAC AGTCAACTCC CTTGGCTTAA TATCAGTAGT AGATATAACCA	840
GAAAGCCAAG GTTTGCATC ACTGAACCTTC TCATCACTTA TAACGCCAGT TAGGCCCCCT	900
AGCAAAC	907

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1232 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

AGAATGCTTA TGCTGAGAAT GAGATGATTG CATTATTTG CATCCGGCAC CATGTAAGGC	60
TTATAGTAAT AACACCGGAA TATGAAGTTA GTTGGAAATT TGGGGAAAGT GAGTGGCCCC	120
TATGTGGAAT TCTTGCGCTG AGGTCCAATC ACTTCCAACC ATGCGCCCCG CTGAATGGTT	180
GCATGATCAC GGCTATTGCT TCAGCACTTG GGAGGCCTGA GGTTGATGTG TTAAATTATC	240
TGTGTAGGCC TAGCACTAAT CACATCTTG AGGAGCTGTG CCAGGGCGGA GGGCTTAATA	300
TGATGTACTT GGCTGAAGCT TTTGAGGCCT TTGACATTG TGCAAAGTGC GACATAAATG	360
GGGAAATTGA GGTCATTAAC CCAAATGGCA AGATTCCGC CTTGTTGAT ATAACTAATG	420
AGCACATAAG GCATGTTGAG AAGATCAGCA ATGGCCCTCA GAGCATAAAA ATAGATGAGT	480
TGAGGAAGGT TAAGCGATCC CGCCTTGACC TTCTTCAAT GAATGGGTCC AAAATAACCT	540
ATTTTCCAAA CTTTGAGCGG GCTGAAAAGT TGCAAGGGTG CTTGCTAGAG GGCCTGACTG	600
GTGTCATAAG TGATGAAAAG TTCAGTGATG CAAACCTTG GCTTCTGGT ATATCAACTG	660
CGGATATTAA GCCAAGAGAG CTAACGTGCG TGCTTGGCAC ATTTGGTGCT GGAAAGAGTT	720
TCTTGTATAA GAGTTTCATG AAGAGATCTG AAGGAAAATT TGTAACCTTT GTTTCCCTA	780
GGCGAGCTT GGCCAATTG ATCAAGAATG ATCTTGAAAT GGATGATGGC TGCAAAGTTG	840
CCAAAGCAGG CAAGTCAAAG AAGGAAGGGT GGGATGTGGT AACATTGAG GTTTCCCTA	900
GAAAAGTTTC TGGTTGAAG GCTGGTCATT GTGTGATTTT CGATGAGGTT CAGTTGTTTC	960
CCCCCTGGATA TATCGATCTA TGTTTACTTG TCATACGCAG TGATGCTTTT ATTCACCTTG	1020

CCGGTGATCC ATGCCAGAGC ACATATGATT CACAAAAGGA TCGGGCAATT TTGGGAGCTG	1080
AGCAGAGTGA CATACTCAGA TTGCTTGAAG GAAAGACGTA TAGGTACAAC ATAGAAAGCA	1140
GACGTTTGT GAACCCAATG TTTGAATTAA GACTACCATG TCACATTCAA AAAGGGTTCA	1200
ATGACTGCTG CCTTGCTGA TTATGCAATC TT	1232

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GCTTCAGCAC TTGGAAGGCG

20

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CACACAGTGG CCAGCCT

17

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GGAGGTGCGT TGTGGTTATG

20

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

CCCTGGCACT GCACACCC

18

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GGAGGTGACC ACATTACG

18

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

CATCACGACT TGTACAAAC C

21

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

TGGGCCTCCA CTTCTTC 17

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GGGGTTGCCT GAAGAT 16

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

ACACCTGCTG TGAAAGC 17

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GGCCAAGGTT CAGTTG 17

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GATGAGGTCC AGTTGTTCC

20

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

ATCCAAAGGA CCTTTTGACC

20

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

CTTGATGAGT ACTTGTC

17

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GCAAGGATTG GGATGGC

17